```
               GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on:  May 11, 2002, 14:47:39 ; Search time 1478.06 Seconds
                                  (without alignments)
                          17934.333 Million cell updates/sec

Title:          US-09-911-513-1
Perfect score:  1964
Sequence:       1 taataatcatttttttctt.........tctaaattactcacactggc 1964

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters:     27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      EST:*
          1:  em_estba:*
          2:  em_esthum:*
          3:  em_estin:*
          4:  em_estmu:*
          5:  em_estov:*
          6:  em_estpl:*
          7:  em_estro:*
          8:  em_htc:*
          9:  gb_est1:*
         10:  gb_est2:*
         11:  gb_htc:*
         12:  gb_gss:*
         13:  em_gss_hum:*
         14:  em_gss_inv:*
         15:  em_gss_pln:*
         16:  em_gss_vrt:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match Length	DB	ID	Description
1	362.6	18.5	626	9	BE204113	BE204113 EST396789
2	360	18.3	376	10	BE525349	BE525349 M7A6STM A
3	342.6	17.4	563	10	BI270025	BI270025 NF003D04F
c 4	333.4	17.0	372	10	234599	234599 ATTS3359 Ve
5	333.4	17.0	457	10	T22782	T22782 4790 Lambda
6	306.4	15.6	1064	9	BE035220	BE035220 MO01E08 M
7	302.2	15.4	743	9	AW774515	AW774515 EST33666
8	298	15.2	343	10	234183	234183 ATTS3217 Ve
9	291.4	14.8	579	9	AW704479	AW704479 sk53e12.y
10	286.8	14.6	579	10	BI498716	BI498716 sai21f11.
c 11	283	14.4	739	12	BH552965	BH552965 BOHUA01TR
12	281.4	14.3	549	10	BM177886	BM177886 saj66f05.
13	281.2	14.3	543	10	BG155663	BG155663 saa64a06.
14	281.2	14.3	700	10	BG587404	BG587404 EST489176
15	277.2	14.1	686	10	BG452287	BG452287 NF083C09L
16	272	13.8	626	9	AI728708	AI728708 BNLGHi114
17	271.2	13.8	438	9	AI993756	AI993756 701497447
18	264	13.4	578	10	BM177413	BM177413 saj81a10.
19	263.8	13.4	716	12	BH483575	BH483575 BOHQX86TR
20	257.4	13.1	671	10	BG443698	BG443698 GA_Ea002
21	255.8	13.0	450	9	AW396192	AW396192 sh02e12.y
22	255	13.0	494	10	BG510374	BG510374 sac76h08.
23	249.8	12.7	636	12	BH456518	BH456518 BOGRX42TR
24	245.4	12.5	511	10	BG790472	BG790472 sae58a03.
25	242.4	12.3	531	10	BG467356	BG467356 00978 lea
26	237.8	12.1	525	10	BF003363	BF003363 EST431861
27	236.6	12.0	524	10	BE329503	BE329503 so66b12.y
28	235.2	12.0	408	9	AV423888	AV423888 AV423888
29	230	11.7	430	9	AV413998	AV413998 AV413998
30	228.8	11.6	501	10	BM358370	BM358370 GA_Ea000
31	227.8	11.6	494	10	BI972280	BI972280 sag89e03.
32	226.6	11.5	610	9	AW585919	AW585919 EST317542
c 33	223	11.4	714	9	AW348855	AW348855 GM210010A
34	219	11.2	563	10	BG043071	BG043071 st91h01.Y
35	218.8	11.1	563	10	BF588097	BF588097 FM1_37_F0
36	218.4	11.1	452	9	AI416823	AI416823 sa18d06.y
37	214.2	10.7	666	12	B62460	B62460 T21N16TF TA
38	211	10.7	436	10	BF324736	BF324736 su14g09.y
39	209.8	10.7	473	9	AW734476	AW734476 sk94h05.y
40	208	10.6	626	10	BF009011	BF009011 ss72c03.Y
41	200.6	10.2	646	12	B62171	B62171 T20L13TF TA
42	195.2	9.9	708	10	BG586497	BG586497 EST488265
43	194.2	9.9	465	9	AL378474	AL378474 MtBB38D11
c 44	193	9.8	427	9	AW310145	AW310145 sf3ig08.x
c 45	191	9.7	321	10	T46205	T46205 9468 Lambda

ALIGNMENTS

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RESULT     1
BE204113
LOCUS       BE204113       626 bp    mRNA    linear   EST 05-SEP-2000
DEFINITION  EST396789 KV0 Medicago truncatula cDNA clone pKV0-14D23, mRNA
            sequence.
ACCESSION   BE204113
VERSION     BE204113.1  GI:8747396
KEYWORDS    EST.
SOURCE      barrel medic.
ORGANISM    Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 626)
AUTHORS     VandenBosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
            Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
            Fraser,C.M.
TITLE       ESTs from uninoculated seedling roots of Medicago truncatula
JOURNAL     Unpublished (1999)
COMMENT     Contact: VandenBosch K
            Department of Biology
            Texas A&M University
            College Station, TX 77843-3258, USA
            Tel: 409 845 7707
            Fax: 409 845 2891
            Email: kate@mail.bio.tamu.edu
            Texas A&M University name:T263885e
            TIGR sequence name:MTGAO24TK
            More information is available at..
            http://chrysie.tamu.edu/medicago
            Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
FEATURES             Location/Qualifiers
     source          1..626
                     /organism="Medicago truncatula"
                     /cultivar="genotype A17"
                     /db_xref="taxon:3880"
                     /clone="pKV0-14D23"
                     /clone_lib="KV0"
                     /tissue_type="Seedling roots"
```

```
                    /dev_stage="Immediately prior to inoculation with
                    Sinorhizobium meliloti (0 hour)"
                    /lab_host="E.coli strain XLOLR"
                    /note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
                    XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
                    was directionally ligated into the Unizap XR vector from
                    Stratagene and packaged using Gigapack III Gold packaging
                    extracts. Plasmids containing cDNA inserts were excised
                    from the recombinant lambda-Zap phage using Ex-assist
                    helper phage and propagated in XLOLR cells."
BASE COUNT       158 a      125 c      148 g      195 t
ORIGIN

Query Match       18.5%;     Score 362.6;   DB 9;     Length 626;
Best Local Similarity   74.9%;   Pred. No. 5.5e-74;
Matches   474;   Conservative   0;   Mismatches   144;   Indels   15;   Gaps   1;

Qy    663  caactcggcatgttgtcctgttgactcgcaggaggaacggtgtgcgtctcgttcacgcgc  722
           ||||||| |  |||| ||  | ||||||| ||  ||| |||| ||| ||||||| | ||||
Db      9  CAACTCGCTACTAATAATGGTGTGGGAGACACAGAGAAAGGTATTCGTCTTGTTCATAGTT   68

Qy    723  tttggcttgcgtcgaagctgttcagaaggagaatctgactgtggcggaagctctggtga  782
           | |||||||| |||||||||||| ||| |||||  | |  | ||||||||||| |||| |
Db     69  TGATGGCTTGTGCTGAAGCTGTTGAACAGAATAATCTAAAGATGGCGGAGGCTTTGGTTA  128

Qy    783  agcaaatcggattcttagctgtttctcaaatcggacgtatgagaaaagtcgctacttact  842
           |  |||||||| | |||| ||| |  | |  || || || |||| |||| |  |||| | |
Db    129  AACAGATCGGATACTTAGCTGTATGCTCATCACAAGAGGTGCTATGAGAAAGTTGCAACCTATT  188

Qy    843  tcgccgaagctcgcgcggcggattacgtctctctccgtcgcgagagtccaatcgacc  902
           ||| ||||| |  | |  || |||||||| ||| || |  |||||||||| |  |||
Db    189  TCGCTGAAGGTTAGCTAGAGAATCTACGGTGTGTTTCC----------ACAGC  233

Qy    903  actctctccgatactcttcagatgcacttctacgacgacttgtcctt atctcaagttcg  962
           | ||||| |||| | |  || |  ||||| |||| |  |||||||||||| | |  |||||
Db    234  ATTCCGTTTCACTTGCGATTCACTTCAGATCCCATTTCTATGAAACTTGTCCTAATCTAAAATTCG  293

Qy    963  ctcacttcacggcgaatcaagcgattctcgaagctttcaaggaggaagaaagagttcatg  1022
           ||||||||||  |||||||||| ||||| |||||||| |||||| |   || | ||||||
Db    294  CTCACTTCACTGCGAATCAAGCTATTCTCAGAGCTTTTCAAGGAAAATCCAGTGTTCATG  353

Qy   1023  tcattgattctctatgagtcaaggtcttcaatgtcgccggcgcttatgcaggtctcttgcgc  1082
           | ||||||| | | |    |||| | | | |||  |||||| |||||||||||| | |||| |
Db    354  TGATTGATTTCTCGATTAATCAAGGGATGCCAGTGCAGTCGCTTATGCAGGCACTTGCTT   413

Qy   1083  ttcgacctggtggtcctcctgtttccggttaaccggaattggtccaccggcaccggata  1142
           | || ||||||||||||||| ||| ||| | |||| |  ||| || |  ||| ||||||
Db    414  TACGTCCTGGTGGTCCTCCTCTTTCGGTTGACCGGTTGACCGGAATCGGACCTCCCGGCCGTCGGATA  473

Qy   1143  atttcgattatctcatgaagttgggtgtaagctggctcattgctgaggcgattcacg  1202
           | ||  | | |   | |||||||||||  ||  |||||||  |  || || |||||||
Db    474  ACTCAGATCATCTTCAACAAGTTGGGTGGCGGAGGCTTGCTCAATTTGCACAAACGATTCATG  533

Qy   1203  ttgagttgagtacagagagattggctaacacttagctgatcttgatgcttcgatgc  1262
           || || ||| | |  | ||||| ||| |  |  || |||||||||||||| || ||
Db    534  TTCAGTTGACTATCTGGTTTGTTGCTAATAGTTTAGCTGATCTTGATGCTTCGATGC  593

Qy   1263  ttgagcttagaccaagtgagattgaatctgttg  1295
           || || ||  | || ||  | | |||  |||||
Db    594  TTGAACTCCGGTCACCGGAAACGAATCTGTTG  626

RESULT 2
BE525349
LOCUS       BE525349                376 bp    mRNA    linear   EST 19-MAR-2001
DEFINITION  M7A6STM Arabidopsis developing seed Arabidopsis thaliana cDNA clone
            M7A6 5', mRNA sequence.
ACCESSION   BE525349
VERSION     BE525349.1  GI:9783327
KEYWORDS    EST.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
```

```
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 376)
  AUTHORS   White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de
            Ilarduya,O., Unizap,J.G., Jaworski,J.G., Ohlrogge,J. and Benning,C.
  TITLE     A new set of Arabidopsis expressed sequence tags from developing
            seeds. The metabolic pathway from carbohydrates to seed oil
  JOURNAL   Plant Physiol. 124 (4), 1582-1594 (2000)
   MEDLINE  20567808
  COMMENT   Contact: Benning, C
            Dept. of Biochemistry & Molecular Biology
            Michigan State University
            224 Biochemistry, Michigan State University, East Lansing, MI 48824
            , USA
            Tel: 517 355 1609
            Fax: 517 353 9934
            Email: benning@msu.edu
            Michigan State University DNA Sequencing Facility Arabidopsis
            Biological Resource Center, The Ohio State University, 309 Botany &
            Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
            6142920603 TEL: 6142929371.
FEATURES             Location/Qualifiers
     source          1..376
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia"
                     /db_xref="taxon:3702"
                     /clone="M7A6"
                     /clone_lib="Arabidopsis developing seed"
                     /tissue_type="seed"
                     /dev_stage="5-13 days after flowering"
                     /lab_host="E.coli"
                     /note="Organ: Developing seed; Vector: pBluescript SK-;
                     Site_1: EcoRI; Site_2: XhoII"
BASE COUNT       84 a       96 c       88 g      108 t
ORIGIN

Query Match       18.3%;     Score 360;    DB 10;    Length 376;
Best Local Similarity   97.3%;   Pred. No. 2.2e-73;
Matches   366;   Conservative   0;   Mismatches   10;   Indels   0;   Gaps   0;

Qy    361  gcttgaagttatgatctcaatgttcaagaagacgatctttccaactcgctactcgagac  420
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||| ||| |
Db      1  GCTTGAAGTTATGATGTCAATGTTCAAGAAGACGATCTTTCCAACTCGCTACTCGATAC   60

Qy    421  tgttcactataatccggcggagctttacacgtggcttgattctatgctcaccgaccttaa  480
           ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db     61  TGTTCACTATAATCCGGCGGAGCTTTACACGTGGCTTGATTCTATGTCTACCGACCTTAA  120

Qy    481  tcctccgtcgtcaaccgagtacgatcttaaagtcattcccggtgacgcgattcctcaa  540
           || | |  | |  |  |  | |||  |  |||| ||||| ||||||||||| |  ||| |
Db    121  TCTTTCTTTTTCTAACCGCGAGTACGATCTTAAAGTCATTCCCGGTGACGCGGATTCTCAA  180

Qy    541  tcagttcgctatcggcttctcgtctaaccaagcgctggaaccaccacacagcgtggtatac  600
           || ||||||| |||  || | |  ||||||||| |||||||||| ||||| | || |||||
Db    181  TCAGTTCGCTATCGGCTTCTCGTCTAACCAAGGCGTCGTGGAAAACCACTACAGCGACGTATAC  240

Qy    601  tacaaacaagcggttgaaatgctcaaacgctcggacgctcggaaccagcggcgggagatacggctga  660
           |||| ||| |||| ||||| ||| ||||| |||  || |  | |||||  | || || ||| |||||
Db    241  TACAAACAAGCGGTTGATATCGTCAAAACGCTCGTGTGGTAACCACTACAGCGACGACGGCTGA  300

Qy    661  gtcaactcggcatgttgtcctgttgactcgcaggagaacggtgtgcgtctcgttcacgc  720
           ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db    301  GTCAACTCGGCATGTTGTCCTGTTGACTCGCACGAGAACGGTGTGCGTCTCGTTCACGC  360

Qy    721  gctttggcttgcgct  736
           || ||||||||||||
Db    361  GCCTTTTGGCTTGCGCT  376

RESULT 3
BI270025
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LOCUS       BI270025               563 bp    mRNA    linear   EST 18-JUL-2001
DEFINITION  NF003D04FL1F1042 Developing flower Medicago truncatula cDNA clone
            NF003D04FL 5', mRNA sequence.
ACCESSION   BI270025
VERSION     BI270025.1  GI:14877244
KEYWORDS    EST.
SOURCE      barrel medic.
ORGANISM    Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 563)
AUTHORS     Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
TITLE       Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula flower library
JOURNAL     Unpublished (2001)
COMMENT     Contact: May GD
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7391
            Fax: 580 221 7380
            Email: gdmay@noble.org
            Insert Length: 563  Std Error: 0.00
            Plate: 003  row: D  column: 04
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1..563
                     /organism="Medicago truncatula"
                     /db_xref="taxon:3880"
                     /clone="NF003D04FL"
                     /clone_lib="Developing flower"
                     /tissue_type="Developing flowers"
                     /dev_stage="Developmentally pooled. Contains a mixture of
                     very young, developing, fully-opened flowers and flowers
                     in early transition into pods."
                     /note="Vector: Lambda Zap; cDNA was prepared from polyA+
                     enriched, pooled samples of equivalent amounts of total
                     RNA from very young, developing, fully-opened flowers and
                     flowers transitioning into pods. The cDNA was
                     directionally ligated into the Uni-Zap XR vector
                     (Stratagene) and packaged using the GigaPack III Gold
                     packaging extracts. Phagemids containing cDNA inserts were
                     in vivo excised from the recombinant Uni-ZAP XR vector
                     using ExAssist helper phage and the E. coli strain
                     XL1-Blue MRF' (Stratagene). Excised plasmids were plated
                     using SOLR cells."
BASE COUNT  139 a   116 c   127 g   177 t   4 others
ORIGIN

Query Match       17.4%;  Score 342.6;  DB 10;  Length 563;
Best Local Similarity  76.1%;  Pred. No. 2.5e-69;
Matches  439;  Conservative  0;  Mismatches 123;  Indels 15;  Gaps 1;

Qy  751 ggagaatctgactgtggcggaagctctggtgaagcaaatcggattcttagctgttctca 810
        | |||||| | ||||||| ||| |||| | |||  | |||||| ||||| || ||
Db    1 GAATAATCTAAAGATGGCGGAGGCTTTGGTTAAACAGATCCGATACTTAGCTGTATCACA 60

Qy  811 aatcggagctatgagaaagtcgctacttacttcgccgaagctctcgcgcgcggcggatta 870
        | |||||||| ||| ||| | ||||| || |  |||| |  |  ||| | |
Db   61 AGAAGGTGCTATGAGAAAAGTTGCAACCTATTTCGCTGAAGGTTTAGCTAGAAGAATCTA 120

Qy  871 ccgtctctccgtcgcagagtccaatcgaccactctctccgatactcttcagatgca 930
        || || | ||||  ||| ||||  |  |  ||| |||||| | |||||||||||
Db  121 CGGTGTGTTCC----------ACAGCATTCCGTTTCCGATTCACTTCAGATCCA 165

Qy  931 cttctacgagacttgtccttatctcaagttcgctcacttcacgcgaatcaagcgattct 990
        ||||| || || || |||| ||| | ||||||| |||||||  | | |||||||||
Db  166 TTTCATGAAACTTGTCCTAATCTAAAATTCGCTCACTTCACTGCGGAATCAAGCTATTCT 225
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```
Qy  991 cgaagctttcaagggaggaagaagagttcatgtcatgtcattgatttctctgtgagtcaaggtct 1050
        ||||||||||| ||  ||  |||||| |||||| |||| |||||||||||||| |||| | |
Db  226 AGAAGCTTTCAAGGAAAATCAGTGGTCATGTTCATGTGATTGATTTCTGATTAATCAAGGGAT 285

Qy 1051 tcaatggccggccgcttatgcagctcttgcggctcgacctggtggtcctccgtttccg 1110
        ||||||||| |||| ||||||| | ||||||  | ||||||||||||| |||| ||||
Db  286 GCAGTGGCGCGGCGTTATGCAGGCACTTGCTTTACGTCCTGGTGGTCCTCCTGCTTTCG 345

Qy 1111 gttaaccggaattggtccaccgcaccggataaatttcgattatcttcatgaagttgggtg 1170
        |||  |||||| || ||  || ||  ||||| | | ||||||||||||||||||||||||
Db  346 GTTGACCGGAATCGGAACTCCGGCGTCGGATAACTCAGATCATCTTCAACAAGTTGGGTG 405

Qy 1171 taagctggctcattagctgagccggattcacgttggttggtacagaggatttggc 1230
        | ||||||||||| ||  |   || |||| |||| |||| |||||| ||  | ||
Db  406 GAGGCTTGCTCAATTTGCACAAGATTCATGTTCAGTTGAGTATCGTGGTTTTGTTGC 465

Qy 1231 taacacttagctgatccttgatgctcgatgcttgagcttagaccaagtgagattgaatc 1290
        ||| | ||||||||||| |||||||| |||||||| || |||| |||| | | |||||
Db  466 TAATAGTTTAGCTGATCTTGATGCTTCGATGCTTGAACTCCGGNCACCGGAAACGGAATC 525

Qy 1291 tgttcggttaactctgtttttcgagcttcacaagctc 1327
        |||| |||  |||||| |||| | || ||||| ||||
Db  526 TGTTGCGGNTAACTCTGNTTTGANCTTCATAAACTC 562
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RESULT  4
Z34599/c
LOCUS       Z34599                  372 bp    mRNA    linear   EST 11-JUL-1994
DEFINITION  ATTS3359 Versailles-VB Arabidopsis thaliana cDNA clone VBVDF10,
            mRNA sequence.
ACCESSION   Z34599
VERSION     Z34599.1  GI:506916
KEYWORDS    EST.
SOURCE      thale cress.
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 372)
AUTHORS     CNRS.
TITLE       The Arabidopsis thaliana transcribed genome: the GDR cDNA program
JOURNAL     Unpublished (1996)
COMMENT     Contact: Desprez T., Amselem J., Chiapello H., Rouze P., Caboche
            M., Hofte H.
            INRA Versailles
            Laboratoire de Biologie Cellulaire
            Route de Saint-Cyr,78026 Versailles Cedex,France
            Email: thierry@versailles.inra.fr.
FEATURES             Location/Qualifiers
     source          1..372
                     /organism="Arabidopsis thaliana"
                     /strain="ecotype Columbia"
                     /db_xref="taxon:3702"
                     /clone="VBVDF10"
                     /clone_lib="versailles-VB"
                     /tissue_type="whole seedlings"
                     /dev_stage="in vitro-grown etiolated seedlings,5 days old"
                     /note="vector: pBluescript"
BASE COUNT  113 a   97 c   73 g   88 t   1 others
ORIGIN

Query Match       17.0%;  Score 333.4;  DB 10;  Length 372;
Best Local Similarity  98.9%;  Pred. No. 3.4e-67;
Matches  356;  Conservative  0;  Mismatches 2;  Indels 2;  Gaps 2;

Qy 1587 agcgtcatgaaacgttg-agtcagtggaggaaccggtcggggttcgcggct 1645
        | ||||||||||||||| |||||||||||||||||||||||   ||||||
Db  359 ACCGTCATGAAACGTTGAAGTCAGTGGAGGAACCGGTCGGGTCGCGGCT 300

Qy 1646 gcacatattggttcgaatgcgtttaagcaagcgagtatgctttggctgttcaacggc 1705
        |||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db  299 GCACATATTGGTTCGAATGCGTTTAAGCAAGCGAGTATGCTTTGGCTGTTGTTCAACGGC 240
```

```
Qy   1706  ggtgagggttatcggggtgggagagtgacgggctgtctcatgttggttggcacacacga  1765
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    239  GGTGAGGGTTATCGGGGTGGGAGAGTGACGGGCTGTCTCATGTTGGTTGGCACACACGA   180

Qy   1766  ccgctcatagccacctcggcttggaaactctccaccaattagatggtggctcaatgaatt  1825
           |||||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||
Db    179  CCGCTCATAGCCACCTCGGCTTGGAAACTCT-CACCAATTAGATGTGGCTCAATGAATT   121

Qy   1826  gatctgttgaaccggttatgatgatgatattccgaccgaagccaaactaatcctactgt  1885
           ||||||||||||||||||||||||||||||| |||||||  |||||||| ||||||||
Db    120  GATCTGTTGAACCGGTTATGATGATGATATTTCGACCGACCGCAAACTAAATCCTACTGT   61

Qy   1886  tttccctttgcacttgttaagatcttatctttcattattataggtaattgaaaaattt  1945
           |||||||||| ||||||||||||||||||||||||||| ||||||||||||||||||
Db     60  TTTTCCCTTTGTCACTTGTTAAGATCTTATCTTTCATTATATTAGGTAATTGAAAAATTT    1
```

RESULT 5
T22782
LOCUS   T22782   457 bp   mRNA   linear   EST 06-NOV-1997
DEFINITION 4790 Lambda-PRL2 Arabidopsis thaliana cDNA clone 107E8T7, mRNA
            sequence.
ACCESSION   T22782
VERSION   T22782.1 GI:2597312
KEYWORDS   EST.
SOURCE   thale cress.
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 457)
AUTHORS   Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh
            ,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel
            ,E. and Somerville,C.
TITLE   Genes galore: a summary of methods for accessing results from
            large-scale partial sequencing of anonymous Arabidopsis cDNA clones
JOURNAL   Plant Physiol. 106, 1241-1255 (1994)
MEDLINE   95148729
COMMENT   On Nov 6, 1997 this sequence version replaced gi:932620.
            Contact: Thomas Newman
            MSU-DOE Plant Research Laboratory
            Michigan State University
            MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
            Lansing,Mi
            Tel: 517-353-0854
            Fax: 517-353-9168
            Email: 22313tcn@ibm.cl.msu.edu
            Seq primer: T7 dye primer.
FEATURES   Location/Qualifiers
     source   1..457
                     /organism="Arabidopsis thaliana"
                     /strain="var columbia"
                     /db_xref="taxon:3702"
                     /clone="107E8T7"
                     /clone_lib="Lambda-PRL2"
                     /note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
                     Lambda PRL2 is a cDNA library derived from equal
                     quantities of 4 pools of mRNA. The mRNA sources were 1) 7
                     day germinated etiolated seedlings; 2) tissue culture
                     grown roots; 3) staged plants half with 24 hour light
                     cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
                     same plants as 3 but aerial tissue (stems, flowers and
                     siliques. The vector is BRL's lambda zip-Lox. The cDNA
                     inserts were directionally cloned with Sal-Not arms using
                     oligo dT primed cDNA."
BASE COUNT   141 a   86 c   87 g   125 t   18 others
ORIGIN

```
Qy     34  ctattttacaatttatttgttattagaagtggtagtggagtggagtgaaaaacaaatcctaa   93
           |||||| |||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db      1  CTATTTTNCAATTTATTTTGTTATTAGAAGTGGTAGTGGAGTGGAGTGAAAAACAAATCCTAA   60

Qy     94  gcagtctaaccgatcccgaagctaaagattcttcaccttcccaaataaagcaaaacct  153
           |||||| |||||||||||||||||||||||| ||||||||||||||||||||||||||
Db     61  GCAGTCCTAACCGATCCCGAAGCTAAAGATTCTNCACCTTCCCAAATAAAGCAAAACCT  120

Qy    154  agatccgacattgaaggaaaaacctttagatccatctctgaaaaaaccaaccatgaa  213
           |||||||||||||||||||||||||||| ||||||||||| |||||||||||||||||
Db    121  AGATCCGACATTGAAGGAAAAACCTTTNGATCCATCTCTG-AAAAAACCAACCATGAA  179

Qy    214  gagag---atcatcatcatcaagataagaagactatgatgaatgaagaga  270
           |||||    |||||||||||||||||||||||||||||||||||||| ||
Db    180  GAGAGATCATCATCATCATCAAGATAAGAAGACTATGATGAATGAAGAAGN  239

Qy    271  cgacggtaacggcatggatggagcttctagctagctgttcttggttacaaggttaggtcatcgga  330
           ||||||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||| |||
Db    240  CGACGGTAACGGCATGGATGGAGCTTCTAGCTGTTCTTGGTTATAAGGTTAGGTCATCCGA  299

Qy    331  aatggctgatg-ttgctcagaaactcgagcagctgaagttatgatgtctaaatgttcaag  389
           |||||||||||  ||||||||||||||||||||||||||||||||||||||| |||||||
Db    300  AATGGCTGATGTTGCTCAGAAACTCGAGCAGCTGAAGTTATGATGTCTAATGTTCAAG  359

Qy    390  -aagacgatctttctcaact--cgctactgagactgttcactataatccgggcgggagctt  446
            |||| ||| ||| ||||||   ||| |||||| ||||||||| ||||| |||| ||| |||
Db    360  NAAGNCGGTCTTTNTCAACTTCCGNACTTNNGACTGTTCACTNTAATNCGGCGGNNGTTT  419

Qy    447  --acacgtggctgattctatgtcaccgaccttaat  481
             |||| ||||| | |||||| | ||||||||||||
Db    420  TCAACGNTGGCTTGNTTTCNATGNTNACCGACCTTAAT  457
```

RESULT 6
BE035220
LOCUS   BE035220   1064 bp   mRNA   linear   EST 07-JUN-2000
DEFINITION MO01E08 MO Mesembryanthemum crystallinum cDNA 5' similar to rgal
            protein, mRNA sequence.
ACCESSION   BE035220
VERSION   BE035220.1 GI:8330344
KEYWORDS   EST.
SOURCE   common ice plant.
ORGANISM   Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1 (bases 1 to 1064)
AUTHORS   Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M., Ferrea
            ,H., Kawasaki,S., McCollough,A., Michalowski,C.B., Palacio,C.,
            Scara,G., Wheeler,M. and Zepeda,G.R.
TITLE   Functional Genomics of Plant Stress Tolerance
JOURNAL   Unpublished (2000)
COMMENT   Contact: Michalowski,C.B.
            University of Arizona
            Bio Sciences West room 513, Tucson, AZ 85721, USA
            Tel: 520-621-7982
            Fax: 520-621-1697
            Email: cbm@u.arizona.edu
            An open reading frame exists.
FEATURES   Location/Qualifiers
     source   1..1064
                     /organism="Mesembryanthemum crystallinum"
                     /db_xref="taxon:3544"
                     /clone_lib="MO"
                     /tissue_type="apical meristem and leaf primordia"
                     /dev_stage="5 weeks"
                     /note="no stress"
BASE COUNT   231 a   225 c   296 g   310 t   2 others
ORIGIN

Query Match   17.0%; Score 333.4; DB 10; Length 457;
Best Local Similarity 90.4%; Pred. No. 3.4e-67;
Matches 414; Conservative   0; Mismatches 33; Indels 11; Gaps   6;

Query Match   15.6%; Score 306.4; DB 9; Length 1064;

Best Local Similarity 68.3%; Pred. No. 7.1e-61; Indels 3; Gaps 1;
Matches 440; Conservative 0; Mismatches 201;

```
Qy 1197 ttcacgttgagttgagtacagagagtttgtgctaacacttagctgatcttgatgctt 1256
        ||| | |||||||| || |||| || |||| ||| ||| ||
Db   38 TCCATATCCAATTTGAGTATCGTGGGTTTGAGCCAATAGTTGACGGATTTGGAATGTT 97

Qy 1257 cgatgcttgagcttagaccaagtgagattgaatctgttcggttaactctgtttcgagc 1316
        |||||| || |  || || |||| ||||| | |||| | ||||||| || ||
Db   98 CGATGCTCGATCTAAGGGCG---GAGACAGAGGCCGCGGCGATCAACTCGGTGTTTGAGC 154

Qy 1317 ttcacaagctcttgggacgacctgtgcgatcgatacaaggttcttggtggtgaatcaga 1376
        |||| ||| ||| |||||  |||||| | |||| ||  |-||||  ||  |-|-|
Db  155 TCCACCGGCTGCTGCCGACCGGGGCGCGTCGAGAAGGTGTTGGGGCTTGTCAAGGAGG 214

Qy 1377 ttaaaccggagatttcactgtgttgagcaggaatcgaaccatatagtccgatttttct 1436
        |||| ||| |||||  |||||  |||||||||| |||| ||| |||| || |||
Db  215 TGAACCCGGTAATCATGACGGTTGTTGAACGACAGGAATCAAACCACAACAGCCCGGGTTCC 274

Qy 1437 tagatcggtttactgactgccattattactcgacgtgtttgactcgttgaaggtg 1496
        || ||| || | | |||| || |||| || || ||||||| ||  || |||| |
Db  275 TAGACCGGTTCAATGAATCCTTGCATTATTCCACCATGTTTGACTCGCTTGAGAGCT 334

Qy 1497 taccgagtggtcaagacaagtcatgtcgagggttacttgggtaaacagatctgcaacg 1556
         |||| |||| |||||| |||  |||||||| | ||||| || |||| |||| ||||
Db  335 GTGTTGACACAACGAGGATAAGATGATGTCGGAGGTGTATCTGGGTAGGCAGATCTGTAACG 394

Qy 1557 ttgtggcttgtgatggaccggacctgagcgtcatgaaaacgttgagtcagtggagga 1616
        | ||||| |||| |||| || ||||||| ||||||| |  ||||||| |||| |||
Db  395 TAGTGGCATGTGAGGGATCAGATCGGTCGGAGAGGCACGAAACGTTGGCCCAATGGAAGA 454

Qy 1617 accggttcggtctgctgggtttggcgctgcacatatggttcgaatgcgtttaagcaag 1676
        |||||||| || ||| | || | |  ||| | |   ||||| ||| ||| |||| |
Db  455 CCCGGTTCGGTTCGGTGCCGGTTTGCACCCGGTTCAACCGGTTCAAATGCGTGTAAGCAGG 514

Qy 1677 cgagtagtgctttggctgctgttcaacggcggtgaggttatcgggtggagagtgacg 1736
        | || |||||| |||| | || |  ||| | ||  | |||| ||||| ||||| |||
Db  515 CAAGTATGCTGTTGGAGTTCTTTGCATGTGGGGATGGCTATGGTGTGGAAGAGAGTGACA 574

Qy 1737 gctgtcctcatgttgggttggcacacacgaccgctcatagcaacgcctcggcttggaaactct 1796
        | |||  ||||||||||||||| |||  | ||| ||||| | || ||||||||| |||||
Db  575 GATGTTTGATGTTGGGTTGGCCACTCACTATGCCACCTCATCACCACCTGGCTTGGCAACTCG 634

Qy 1797 ccaccaattagatggtggctcaatgaatcagttgacctgttgaaccgg 1840
        ||  |  || ||| |||| ||||| |||| |||  |||||||||||||
Db  635 CCAAGAAATCGCCAACTCGGCGCGTGAGTCGCTGTTTAACTCGG 678
```

RESULT 7
AW774515

Query Match   15.4%;   Score 302.2;   DB 9;   Length 743;
Best Local Similarity   68.3%;   Pred. No. 6.6e-60;
Matches 453;   Conservative 0;   Mismatches 198;   Indels 12;   Gaps 2;

```
Qy  833 gctacttacttcgccgaagctccgccgcggccggattaccgtctctctccgtcgcagagt 892
        ||  |  | |||||| ||| ||||| || |  |  ||||| |||    ||  |  |
Db    1 GCTTCCTATTCGCCACAAGCACTTGCAAGAAGAAATCTACGGTAAC------CCAGAAGAA 54

Qy  893 ccaatcgaccactctctccgatactctcagatcttcagatcgacttgtcctat 952
        |||||||| |||| |  |   || ||||| ||  | ||||| |  || ||||||
Db   55 ACAATCGATTCATCATTCTTCAGAAATTCTTCACGACACTTCTATGAATCTTCACCTTAT 114

Qy  953 ctcaagttcgctcactcacggcgaatcaagcgatctcgaagcttttcaagggaagaaa 1012
        |||||||||||| ||| ||| |||||||||| | | ||||||||| | ||||| |||||
Db  115 CTCAAATTCGCTCATTTCACTGCTAATCAAGCTATTCTCGAAGCTTTCGCCGGTGCCGGA 174

Qy 1013 agagttcatgtcattgatttctctatgagtcaagtgtctcaatggccggcggcgcttatgcag 1072
        ||||||||||| ||| | ||| |||||||||||||  |  | |||||||| || ||||||||||
Db  175 AGAGTTCATGTTATTATAGATTTTGGCTTAAACAACGGATGCAATGGCCTGCGCTTATGCAA 234

Qy 1073 gtcttgcgcttcgccgaccggtggtgtcctcctgtttccggttcaccggttaccaccg 1132
        ||| || | || |  |  || |||||| |  |  ||| |||||||| | |||| ||||||
Db  235 GCGCTGGCCATTACGTCCTCGGCCGGTCCTCCTCACGTTCCGGTTAACCGGCATCGGACCGCCG 294

Qy 1133 gcaccggataatttcgattatctttcatgaagttgggtgtaagctggctcattagctgag 1192
        | | ||| ||||| |||| |  || || |||| ||||| |||| ||||| | |||||||
Db  295 CAGGCGGACAATACTGATGCTTTGCCAACAAGTTGGCTGGAAATTAGCTCAGCTTGCTCAG 354

Qy 1193 gcgattcacgttgagttgagtacagagagatttgtggctaacacttagctgatcttgat 1252
        | | |||| ||| ||||||||| |||||| | |||||| |||| | ||| || |||| |
Db  355 ACAATCGGTGTTCAGTTCGAATTTCGTGGATTTCTTGTGAACAGTATTGCGGATCTTGAC 414

Qy 1253 gcttcgatgctgagcttagaccaagtgagattgagattgaatctgttcggttaactctgtttc 1312
        | | |||||||||| |||||||   |  ||||||    |  ||| ||| || |||| || |||
Db  415 CCGAATATGCTTGAGATCCGACCCCG------TGAAGCTGTTGCTGTTAACTCCGTTTTTC 468

Qy 1313 gagcttcacaagctcttgggacgacctgtgcgatcgataaggttcttggtgtggtgaat 1372
        ||||||||   || |||| | ||||| |  |||| |||| ||| ||| | || ||| |
Db  469 GAGCTTCATACCATTGGTTAGCTCGACCCGGTTCAGTTGAGAAGTTCTCAACACTGTTAAG 528

Qy 1373 cagattaaacccggagatttcactgtggttggacgaggatcgggaccataatagtccgatt 1432
        ||||| |||||  || |||||||||| |||| ||| | ||| | ||||||  ||| |||||
Db  529 AAGATAAACCCTAAAATCCTAAAATCGTTAGACAATCGTTGAGCAAGAAGAGCGAATCATAACGGACCGGTT 588
```

```
Qy  1433  tccttagatcgagtcgttactgagtcgttgcattattaccgacgttgttgactcgttggaa  1492
          ||| |||| |||| ||||||| ||   ||  |||||| |||   || || |||  ||||||
Db   589  TTCGTAGACCGGTTACCGAAGCTTTACATTATTACTCAAGCTTATTCGATTCACTCGAG     648

Qy  1493  ggt  1495
          |||
Db   649  GGT  651
```

RESULT   8
Z34183
LOCUS   Z34183   343 bp   mRNA   linear   EST 14-JUN-1994
DEFINITION ATTS3217 Versailles-VB Arabidopsis thaliana cDNA clone VBVDF10,
            mRNA sequence.
ACCESSION   Z34183
VERSION   Z34183.1   GI:498540
KEYWORDS   EST.
SOURCE   thale cress.
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 343)
AUTHORS   CNRS
TITLE   The Arabidopsis thaliana transcribed genome: the GDR cDNA program
JOURNAL   Unpublished (1996)
COMMENT   Contact: Desprez T., Amselem J., Chiapello H., Rouze P., Caboche
            M., Hofte H.
            INRA Versailles
            Laboratoire de Biologie Cellulaire
            Route de Saint-Cyr,78026 Versailles Cedex,France
            Email: thierry@versailles.inra.fr.
FEATURES   Location/Qualifiers
     source   1..343
                     /organism="Arabidopsis thaliana"
                     /strain="ecotype Columbia"
                     /db_xref="taxon:3702"
                     /clone="VBVDF10"
                     /clone_lib="Versailles-VB"
                     /tissue_type="whole seedlings"
                     /dev_stage="in vitro-grown etiolated seedlings,5 days old"
                     /note="Vector: pBluescript"
BASE COUNT   86 a   79 c   92 g   85 t   1 others
ORIGIN
Query Match   15.2%;   Score 298; DB 10;   Length 343;
Best Local Similarity 97.1%;   Pred. No. 6e-59;
Matches 335;   Conservative   0;   Mismatches   0;   Indels   4;   Gaps   3;

```
Qy   500  gagtacgatcttaaagctattcccggtgacgcgattctcaatcagttcgctatcgattcg  559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  GAGTACGATCTTAAAGCTATTCCCGGTGACGCGATTCTCAATCAGTTCGCTATCGATTCG   60

Qy   560  gcttcttcgtctaaccaaggcgcggcggaggagatacgtatactacaaacaagcggttgaa  619
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GCTTCTTCGTCTAACCAAGGCGCGGCGGAGGAGATACGTATACTACAAACAAGCGGTTGAAA  120

Qy   620  tgctcaaacggcgtcgtggaaaccaccacagcgacggctgag-tcaactggcatgttgt   678
          ||||||||||||||||||||||||||||  ||||||||| |||  |||||| ||||||||
Db   121  TGCTCAAACGGCGTCGTGGAAACCACCACTACAGCGACGGCGCTGAGATCAACTCGGCATGTTGT  180

Qy   679  cctggttgactcgcaggagaaacgtgtgctcgttcacgcgctttggcttgcgctg-    737
          |||||||||||||||||||||  ||||||  |  |||||||||||  |||| ||||
Db   181  CCTGGTTGACTCGCAGGAGAACGGTGTGCCGTCTCCGTTCACGCGCTTTTGCGTTCGCTGA   240

Qy   738  aagtgttcagaaggagaatctgactgtggcggaagtctgtggaagcaaatcggattct   797
          ||| ||||||||| |||||||||||||| |||||  |||||||||||||||||||||
Db   241  AAGCTGTTCAGAAAGAGAATCTGACTGTAGCGGA--NTCTGGTGAAGCAAATCGGATTCT   298

Qy   798  tagctgtttctcaaatcggagctatgagaaagtcgctacttact   842
          |||| |||||||||||||||||| ||||| || ||||||||||||
Db   299  TAGCCGTTTCTCAAATCGGAGCGATGAGAAGAAAGTCGCTACTTACT  343
```

RESULT   9
AW704479
LOCUS   AW704479   579 bp   mRNA   linear   EST 03-DEC-2001
DEFINITION sk53e12.y1 Gm-c1019 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
            Gm-c1019-6311 5' similar to TR:O23724 O23724 GAI GENE. [1] ;, mRNA
            sequence.
ACCESSION   AW704479
VERSION   AW704479.1   GI:7588689
KEYWORDS   EST.
SOURCE   soybean.
ORGANISM   Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1 (bases 1 to 579)
AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.
            ,Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
TITLE   Public Soybean EST Project
JOURNAL   Unpublished (1999)
COMMENT   Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            Insert Length: 1731   Std Error: 0.00
            Seq primer: -40RP from Gibco
            High quality sequence stop: 424.
FEATURES   Location/Qualifiers
     source   1..579
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1019-6311"
                     /clone_lib="Gm-c1019"
                     /tissue_type="immature seed coats of greenhouse grown
                     plants"
                     /lab_host="DH10B (Gibco BRL)"
                     /note="Vector: pSPORT1 (Life Technologies); Site_1: Not I;
                     Site_2: Sal I; This cDNA library was constructed from mRNA
                     isolated from immature seed coats (200-300 mgs) of
                     greenhouse grown plants. The library was prepared using
                     the Life Technologies pSuperScript cDNA library
                     construction kit. Complementary DNA was synthesized from
                     mRNA using a poly (dT) sequence with a Not I restriction
                     site. Sal I linker adapters were ligated to the
                     blunt-ended cDNA fragments followed by Not I digestion.
                     The cDNA fragments were directionally cloned into the Not
                     I-Sal I restriction site of the pSPORT1 vector. The
                     ligated cDNA fragments were transformed into E.coli
                     ElectroMax DH10B host cells (Gibco BRL). This library was
                     constructed by Dr. Lila Vodkin and Dr. Anu Khanna."
BASE COUNT   123 a   175 c   173 g   108 t
ORIGIN

Query Match   14.8%;   Score 291.4; DB 9;   Length 579;
Best Local Similarity 73.3%;   Pred. No. 2.2e-57;
Matches 392;   Conservative 0;   Mismatches 131;   Indels 12;   Gaps 1;

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Qy   654  cggctgagtcaactcggcatgttgtcctggttgactcgcaggagaaacggtgtgcgtctcg  713
          || |||||||||  |  ||  | |  |||||||||||||||||||||||  ||| | | ||||
Db    56  CCGACGAGTCAAGCGCGCCGGCGTGGTGGTCGTTGACTCGGAGGAGAACGGGGATCCGCCCTCG  115
```

/clone="GENOME SYSTEMS CLONE ID: Gm-c1053-4101"
/clone_lib="Gm-c1053"
/tissue_type="Whole seedling, 3 week old, greenhouse
grown"
/lab_host="DH10B"
/note="vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The Harosoy NIL was constructed and seed was
provided by Dr. J. Specht, University of Nebraska
(Shoemaker and Specht, 1995). The cDNA library was
constructed from mRNA isolated from whole seedlings of 3
week old greenhouse grown plants. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site and a 3'
anchor. EcoRI adapters were ligated to the blunt-ended
cDNA fragments followed by XhoI digestion. The cDNA
fragments were directionally cloned into the EcoRI-XhoI
restriction site of the pBluescript vector. The ligated
cDNA fragments were transformed into DH10B host cells
(GibcoBRL). This library was constructed in cooperation
with Dr. Paul Keim's laboratory at Northern Arizona
University."

BASE COUNT   119 a   174 c   171 g   115 t
ORIGIN

Query Match   14.6%;   Score 286.8; DB 10; Length 579;
Best Local Similarity   70.7%;   Pred. No. 2.5e-56;
Matches   413; Conservative   0; Mismatches 162; Indels   9; Gaps   2;

```
Qy     962  gctcacttcacggcgaatcaagcgattctcgaagcttcaaggagaaagagttcat 1021
            || |||||||||| || |||  ||||||  | |||||||||  ||||| || |||
Db       1  GCACACTTCACCGCGAACCAGGTTATCCTCGAAGCGTTCCAAGGAAGAACCGCGTTCAC   60

Qy    1022  gtcattgatttcttctatgagtcaaggtcttcaatggccggcggctcctcatttcagg 1081
            || ||||||||  |||||||| || ||  ||||||||||||  |||| | || |||
Db      61  GTGATTGATTTCGTATCAACCAGGGGATGCAGCTACAACCAGGATCCAAGCCTAGCG  120

Qy    1082  cttcgacctggtgtcctcctgtttccggttaaccggatggtccaccggcaccggat 1141
            ||| ||| ||||| |||||||| || ||| ||| ||||| ||| |  || |||||
Db     121  GTTCGCACCGGGGTTCCTCCGGTTTTCCGACTCCACCGGAATCGGGCCGGCGGCGGAC  180

Qy    1142  aatttcgattatcttcatgaagttgggatgggctggctcatttagctgaggcgattcac 1201
            || ||| || ||  |||||| || ||  ||||| ||||  | || |||| | |||
Db     181  AACTCCGACCACCTCCAGGAGGTAGGGTGGAAGCTGGCGGCAGCTGGCGGAGGAGATCAAC  240

Qy    1202  gttgagttgagtacagaggatttgtgctaacactttagctgatcttagctgatcttcgatg 1261
            || ||| ||||| || ||| ||| || || ||||  | ||  |||  | ||||| |
Db     241  GTGCAGTTCGAGTACCGTGGCTTCGTCGGCGAACAGCCTGCCGATCTCGACGGCTCCATG  300

Qy    1262  cttgagcttagaccaagtgagatttgaatcgtgtcggttaactcgtgttcgagctcac 1321
            || ||| ||  |    |||||| || |||   ||| ||| | || ||| | |||||
Db     301  CTCGATCT------CCGGGAAGGCGAAGCCGTCGCTGTGTGAACTCGTCGTTCGAGTTCAC  354

Qy    1322  aagctcttgggacgacctggtgcgatcgataaggttcttggtggtgaatcagattaa 1381
            ||||| |  ||| ||   ||| ||| ||  || ||| ||||| ||||  |||||||
Db     355  AAGCTCCTCGCGCCCGCCCGGCGGGTGGAGAAAGTACTCTCCGTCGTACGGCAGATTCGG  414

Qy    1382  ccgagatttcactgtgttgagcagcaggaatcgaaccacataatagtccgatttcttagat 1441
            |||||||| |||| || || || |||  ||| ||  | |||| || |  || |||  | |
Db     415  CCGGAGATTGTCACCGTCGTCGAGCAAGCGAACAAGCGAACCACAACAGACTGAGTTTTGTCGAC  474

Qy    1442  cggttactgagtcgtcgttgcattattaccgacgttgtttgactcgttggaaggtgtacc- 1500
            |||||| ||||| |||| ||| |||||||  || |||| ||| ||| | || |||
Db     475  CGGTTCACGGAGTCACTGCACTATTATTCAACCCTATTCGACTCGACTGCTGGAGGGTTCGCCT  534

Qy    1501  --gagtgtcaagacaaggtcatgtcggagggtttacttggtaa 1542
              | | ||||||  ||| |||||||||||||||||| ||
Db     535  GTGAACCCTAACGATAAGGCCATGTCCGGAGGTTTACTTAGGGAA  578
```

RESULT 11
BH52965/c
LOCUS   BH552965   739 bp   DNA   linear   GSS 14-DEC-2001

(left column, rotated)

```
Qy    714  ttcacgcgctttggcttggctggctgaagctgtcagaggagaaatctgactgtggcggaag 773
           | |  | |||| || ||||||   | ||||  |||  |   | |||  | ||| ||| ||
Db    116  TGCACAGCCTCATGCGGCTGCGCGGAGGCCGTGGAGAACAACAAAccTCGCCGTGGCGGAGG  175

Qy    774  cctggtgaagcaaatcggattcttagctgtttccaaatcggagctcatgagaaaagtcg 833
           | ||||| || ||| ||  |||| || || ||||| || ||  ||| | ||||||| |||
Db    176  CGCTGGTGAAGCAGATGCGGCTCCTCGGTCGCAGGTTCGAGCTCATGAGGAAAGTCG  235

Qy    834  ctacttacttgccgaagctcgcgcggcggattaccgtctctccgtcgcagagtc 893
           | ||||| ||||| |||||||   ||| ||   | ||| ||  ||  || || ||
Db    236  CAATCTACTTCGCGAAGCGCTGCGAGGCGTCTACAGAGTCTTCCCTCGC------ 289

Qy    894  caatcgaccactcctcctccgatactcttcagatgcagcttctacggactgtccttatc 953
           ||| || ||| | | ||| |  | |||| |||| | |||  | ||| |||| | |||| |
Db    290  ----AACACTCTCTCTCCGATTCTTCTTCAGATTCACTTCACGGAAACCTGCCATACC 343

Qy    954  tcaagttcgctcacttcacgcgcgaatcaagcgattctgaagcttcaagggaagaaaa 1013
           |||||| || |||||||| ||||||| |||||  |||| || ||| |   ||| ||||
Db    344  TCAAGTTCGCACACTTCACCGCGCGAACCAGGTTATCCTCGAAGCGTACCAAGGAAAGAACC 403

Qy   1014  gagttcattgtgtcattgatttctctatgagtcaaggtcttcaatggccggccgcgcttatgcagg 1073
           ||||| || | ||  |||||   || | | ||  ||| | |||| ||   | |||| |||  |||
Db    404  GCGTTCACGTGATTGATTTCGTATCAACCAGGGGATGCAGCTACAACCAGGATCCAAGCCTAGCCAAG 463

Qy   1074  tccttggcttcgaccctggtgtgtcctcctgtttccggttaaccggaattggtccaccgg 1133
           | | |  | ||| |||  || |||   ||  ||| |||| ||  |    || |||| |||
Db    464  CCCTAGCGGTTCGCACCGGGGGTTCCTCCGGTTTTCCGACTCCACCGGAATCGGGCCGGCGG 523

Qy   1134  caccggataatttcgattatcttcatgaagttgggtgtaagctggctcattagc 1188
           | | || |  | |||  ||| || || | |  || | |  | || || |||  |
Db    524  CGGCGGCAACTCCGACCACCTCCAGGAGGTAGGGTGGAAGCTGGCTCGGCCAGCTGGC 578
```

RESULT 10
BH498716
LOCUS   BH498716   579 bp   mRNA   linear   EST 30-NOV-2001
DEFINITION   sai21f11.y1 Gm-c1053 Glycine max cDNA clone GENOME SYSTEMS CLONE
                ID: Gm-c1053-4101 5' similar to TR:O23642 O23642 RGA1 PROTEIN. [1]
                ;, mRNA sequence.
ACCESSION   BH498716
VERSION   BH498716.1 GI:15338060
KEYWORDS   EST.
SOURCE   soybean.
  ORGANISM   Glycine max
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                Glycine.
REFERENCE   1 (bases 1 to 579)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
                ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
                Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
                ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
                ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
                ,R., Waterston,R. and Wilson,R.
  TITLE   Public Soybean EST Project
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Shoemaker R/Public Soybean EST Project
                Public Soybean EST Project
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                Tel: 314 286 1800
                Fax: 314 286 1810
                Email: est@watson.wustl.edu
                This clone is available through: ResGen, Invitrogen Corp. 2130
                South Memorial Parkway Huntsville, AL 35801 For further information
                call: (800)-533-4363 or contact via email: ccu@resgen.com
                High quality sequence stop: 421.
FEATURES   Location/Qualifiers
     source   1..579
                     /organism="Glycine max"
                     /db_xref="taxon:3847"

```
Qy   699 acggtgtgcgtcctcgttcacgcgctctttggcttggctgagctgttcagaaggagaatc 758
         ||||||||| || |||||||| | |||||||| ||||| |||||| | ||||| | ||
Db   261 ACGGTGTGCGGCCTAGTCCACGCGCCTCATGGCCTGCGCGGAAGCTATCCAGAACAACGATT 202

Qy   759 tgactgtggcggaagctcctggtgaagcaaatcggattcttagctgtttctcaaatcggag 818
         | || |||||||||||||||| || |||||| ||||||||||||| ||||||||||||
Db   201 TGTCTATAGCGGAAGCTCTCGTCAAGCAGATTGGATTCTTGGCCGTGTCTCAAGCCGGAG 142

Qy   819 ctatgagaaagtcgtcacttacttcgccgaagctcgcgcggccgattaccgtcct 878
         | ||||| |||||||| || || |||| |||||||||||||||||||| |||| ||||
Db   141 CCATGGAGGAAGTGGCGACGTACTTCGCCGAAGCTCTCGCCGGCCGGATCACCGCCTCT 82

Qy   879 ctccgtcgcagagtccaatcgaccacctctctccgatactcttcagatgcacttcacg 938
         |||| ||||| |||||||| || |||||||||| || || |||||||||||||||||
Db    81 CTCCGCCGCAGACTCAGATCCGATCACTCTCTCCGGACACCGCTCCAGATGCACTTCTACG 22

Qy   939 agacttgtccttatctccagt 959
         ||| ||| |||||||| ||||||
Db    21 AGACGTGCCCTTACCTCAAGT 1
```

```
RESULT 12
BM177886
LOCUS       BM177886                549 bp    mRNA    linear    EST 06-DEC-2001
DEFINITION  saj66f05.y1 Gm-c1072 Glycine max cDNA clone SOYBEAN CLONE ID:
            Gm-c1072-4857 5' similar to TR:O23642 O23642 RGA1 PROTEIN. [1] ;,
            mRNA sequence.
ACCESSION   BM177886
VERSION     BM177886.1  GI:17401104
KEYWORDS    EST.
SOURCE      soybean.
ORGANISM    Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 549)
AUTHORS     Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R. Waterston,R. and Wilson,R.
TITLE       Public Soybean EST Project
JOURNAL     Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact: ccu@resgen.com web site:
            www.resgen.com
            Seq primer: -40RP from Gibco
            High quality sequence stop: 421.
FEATURES             Location/Qualifiers
     source          1..549
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="SOYBEAN CLONE ID: Gm-c1072-4857"
                     /clone_lib="Gm-c1072"
                     /tissue_type="seedlings induced for symptoms of SDS
                     (Sudden Death Syndrome) disease"
                     /dev_stage="2-3 weeks old"
                     /lab_host="DH10B"
                     /note="vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library wms constructed from mRNA isolated
                     from 2-3 week old seedlings that were induced for symptoms
                     of SDS (Sudden Death Syndrome) disease by the
                     translocation of culture filtrate of Fusarium solani f.
```

```
DEFINITION  BOHUA01TR BOHU Brassica oleracea genomic clone BOHUA01, DNA
            sequence.
ACCESSION   BH552965
VERSION     BH552965.1  GI:17804745
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
ORGANISM    Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 739)
AUTHORS     Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE       Whole genome shotgun sequencing of Brassica oleracea
JOURNAL     Unpublished (2001)
COMMENT     Other_GSSs: BOHUA01TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1..739
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOHUA01"
                     /clone_lib="BOHU"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT       166 a    197 c    203 g    173 t
ORIGIN
```

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Query Match         14.4%;   Score 283;  DB 12;  Length 739;
Best Local Similarity   67.5%;   Pred. No. 2e-55;
Matches  500;  Conservative  0;  Mismatches 185;  Indels 56;  Gaps  5;

Qy   273 acggtaacggcatggatgagcttctagctgttcttggttacaaggttaggtcatcggaaa 332
         ||||     ||||||||||||||||||||| |||||     || |||||||||| |||
Db   739 ACGGGCCGAACCATGGATGAGCTTCTCCGCTGTCGTGGGGTACAAAGGTGAGGTCGTCAGAGA 680

Qy   333 tggctgatgttgctcagaaactcgagcagctgagtttatgatgtctaatgttcaaggag 392
         ||||| |||||| ||||||||||| ||| || || ||||| ||||| | |||||||||
Db   679 TGGCCGGAGGTTGCGTTGAAGCTAGAGCAGTTAGAGACCATGATG-GTACGTTTCAAGAAG 621

Qy   393 acgatcttttctcaactcgctactgagacttgtcactataatccgccggagctttacacgt 452
         ||| | ||| |   |||||||||| |||||||| || ||||||||||||||  ||  ||||
Db   620 ATGGT-TATCTAATCTCCGACACGGATACTGTTCACTACACCCGTCGGAGCTTTACTCGT 562

Qy   453 ggcttgattctatgctcaccgaccttaatcctccgtcgtc---------------- 492
         ||||||     |||||| ||| ||||  || || || || ||
Db   561 GGCTTGATAACATGCTCACCGAGTTTAACCCCGCCGCCGGAGATAAACAACTTCGTTTC 502

Qy   493 ------------taacgccgagtacgatcttaaagctattcccggtgacgcgatt---- 535
                     ||||| || ||| |||||| || || ||||| || |||||||||
Db   501 TCGCCCGAGCTGGTGGTGTGCGTTCCGATTACGGACCTCAAAGCCATTCCTGAAACCGGATTTACG 442

Qy   536 -----ctcaatcagttcgtcatcgattcggcttcttcgtctaaccaaggcggcggaggag 590
              ||||  ||||| || |||| ||||||||| ||| |||||| |||||| |||||||
Db   441 CGAGATCCAACCAGTTCGGCGATAGATTCTTCCTCCGTCGAACCAAGCTGGTGATAACA 382

Qy   591 atacgtatactacaaacaagcggttgaaatgctcaaacggcgtcgtggaaac-------- 642
         || |||| || | ||||| ||||| |  |||||||| || || |||  ||
Db   381 GCCAGAGCACCAAGCGTTGAAGTCATGCATGCTCGAGCCCTGATTCGTTGGTTACAGGAACAA 322

Qy   643 ---caccacagcgacggcgtcaactcggacatgttgcctggttgactcgcaggaga 698
            |||| ||   || ||  || |||||||| ||| ||||||  ||||||||||||
Db   321 CGGTAACAACCACAACTATTGAGTCAACTCGGTCCATGTCCTGGGACTCGCAAGAGA 262
```

```
ACCESSION   BG155663
VERSION     BG155663.1  GI:12689327
KEYWORDS    EST.
SOURCE      soybean.
ORGANISM    Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 543)
AUTHORS     Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
TITLE       Public Soybean EST Project
JOURNAL     Public Soybean EST Project
            Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            High quality sequence stop: 419.
FEATURES             Location/Qualifiers
     source          1..543
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1060-1188"
                     /clone_lib="Gm-c1060"
                     /tissue_type="Root, 2 week seedlings"
                     /lab_host="DH10B"
                     /note="vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library was constructed from mRNA isolated
                     from root tissue of 2 week old seedlings for PI468916.
                     Complementary DNA was synthesized from mRNA using a primer
                     consisting of a poly(dT) sequence with a XhoI restriction
                     site. EcoRI adapters were ligated to the blunt-ended cDNA
                     fragments followed by XhoI digestion. The cDNA fragments
                     were directionally cloned into the EcoRI-XhoI restriction
                     site of the pBluescript vector. The ligated cDNA fragments
                     were transformed into DH10B host cells (Gibco BRL). This
                     library was constructed in the laboratory of Dr. Randy
                     Shoemaker at Iowa state university."
BASE COUNT    112 a    169 c    155 g    107 t
ORIGIN
```

```
Query Match             14.3%;    Score 281.2;  DB 10;  Length 543;
Best Local Similarity   71.08%;   Pred. No. 5.1e-55;
Matches 389;  Conservative  0;  Mismatches 153;  Indels  6;  Gaps  1;

Qy    948  cttatctcaagttcgctcacttcacgcgaatcaagcgattctcgaagctttcaaggga 1007
           |||| ||||| ||||| ||||| ||||||||||||||||||||| |||||||| ||||||
Db      2  CTTACCTTAAGTTCGCGCACTTCACCGCAAACCAGGCGATTCTCGAAGCGTTTCAAGGGA   61

Qy   1008  agaaagagttcatgtcattgatttctctatggtcaaggtcttcaatggcggcgctta 1067
           || ||||||||||| ||| |||||| ||||||||||||||||||| ||||||| || ||
Db     62  AAAATCGCGTTCACGTGATTGATTTCGGAATCAACCAGGGATGCAGTGGCCGGCCACTGA  121

Qy   1068  tgcaggctcttgcgcttcgacctggtggtctcctgtttccggttaaccggaattggtc 1127
           ||| |||| ||||| ||||||||||||||||| ||  ||||  || ||||||||| |||
Db    122  TGCAAGCCCTTGCGCTTCGCAACGACGCGCCCCTCCGGGTTTCCGGCTAACCGAATCGGAC  181

Qy   1128  caccggcaccggataattcgattactcatcagaagttggtgaagctggtcatttag 1187
           ||||||| ||| ||| ||| ||| |||| |||||||||||||||||| || |||| ||
Db    182  CGCCGGCGGGCGGACAACTCCGACCACCTCCAGGAGGTAGGGTGGAAGCTCGCCAGCTGG  241
```

```
BASE COUNT    109 a    175 c    152 g    113 t
ORIGIN
```

```
Query Match             14.3%;    Score 281.4;  DB 10;  Length 549;
Best Local Similarity   71.88%;   Pred. No. 4.6e-55;
Matches 404;  Conservative  0;  Mismatches 141;  Indels 18;  Gaps  2;

Qy    806  tctcaaatcggagctatgagaaagtcgctacttacttcgcgaagctctcgccggcgg 865
           || || ||||||||||| ||||||| |||||| ||||| | |||||||||| ||| |||
Db      1  TCGGCAGGTTGGAGCTATGAGGAAAGTCGCAATCTACTTCGCCGAAGCGCTCGCCGAGGCGA   60

Qy    866  atttaccgtctctccgtcgcagagtccaatcgaccactctctccgatactcttcag 925
           || ||                                        CACTCTCTCCGATTCTCTTCAG  108
Db     61  ATCTACAGAGTCTTCCCTCTGCAA----------

Qy    926  atgcacttcacgagactgtccttatctcaagttcgctacttcgctcacttcacggcgaatcaagcg 985
           ||||||||||||| |||| || ||||||||||||||||| |||| | |||||| |||| ||
Db    109  ATTCACTTCTACGAAACCTGTCCATACCTCAAGTTCGCACACTTCACCGCGAAACCAGGTT  168

Qy    986  atttctgaagctttcaaggggagaaaagagttcattgtcattgatttctctatgagtcaa 1045
           || |||||||||| || |||||||||||| |||||  ||| ||||| ||||||| ||
Db    169  ATCCTCGAAGCGTTCCAAGGAAGAAAGAAACCGCGTTCACCGTGATTGATTTCGGTATCAACCAG  228

Qy   1046  ggtcttcaatgccggcgcttatgcaggctctgcaggctcgacctggtggtcctcctgtt 1105
           || | |||||||||||| ||||| ||| ||| |||| |||||||||||||| ||||| |||
Db    229  GGGATGCAGTGGCCGGCCACTGATGCAAGCCCTAGCGGTTCGCACCGGCGTCCTCCGGTT  288

Qy   1106  ttccggttaaccggaattggtccacccggcaccggataattcgatttactcttcatgaagtt 1165
           |||||||  || || ||||||| ||  ||||  || ||| |||| ||| |||| |||||||
Db    289  TTCCGACTCACCGGAATCGGACCGCCGGCGGGCGGACAACTCCGACCACCTCCAGGAGGTA  348

Qy   1166  ggggtgaagctgctcatttagctgagcgattcagcgttgagtttgagtacagagaggattt 1225
           |||| |||||| ||| |||| ||| ||| | ||| | ||||| || |||| || ||||| ||
Db    349  GGGTGGAAGCTCGCCAGCTGGGCGGAGATCAACGTGCAGTTCGGTATGCACCGTGGCTTC  408

Qy   1226  gtggctaacacttagctgatcttgatgcttgatgctgttgaccaagtgagatt------CCCGGAAGGC 1285
           ||||||||| | ||| ||| ||| |||||| |||| |||                    ||
Db    409  GTGGCGGAACAGCCTCGCGATCTCGACGCCTCGCGATCT---------CCCGGAAGGC  462

Qy   1286  gaatctgttgcgtaactctgtttgagctcacaagctcttgggacgacctggtgcg 1345
           || ||||||||| |||| |||| |||| | |||||| |||| ||| ||||| |||
Db    463  GAAGCCGTCGCGTCGTGAACTCTGTCTTCGAGTTTCACAGAGCTCCTCGCGCCGGCCGCG  522

Qy   1346  atcgataaggttcttggtggt 1368
           || ||| ||| ||| || |||
Db    523  GTGGAGAAAGTACTCTCCGTCGT  545
```

```
RESULT 13
BG155663
LOCUS       BG155663      543 bp    mRNA   linear     EST 28-NOV-2001
DEFINITION  saa64a06.y1 Gm-c1060 Glycine max cDNA clone GENOME SYSTEMS CLONE
            ID: Gm-c1060-1188 5' similar to TR:O23642 O23642 RGA1 PROTEIN. [1]
```

```
;, mRNA sequence.
```

sp. glycines (Plant Cell Report 18:375-380). Cultivar PI
567374 is partially resistant to the disease SDS. Plant
tissue (expanded leaves, folded leaves, and new shoots)
were collected at 1, 6, 24, and 48 hrs. after inoculation
and their mRNA pooled equally for cDNA construction. The
library was prepared using the Stratagene pBluescript II
SK(+) library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with an XhoI restriction site. EcoRI
adaptors were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA insert is protected
from XhoI digestion via methylation during first strand
synthesis. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
E.coli ElectroMax DH10B host cells. Plants were inoculated
by Shuxian Li (Glen Hartman lab, University of Illinois).
Library was constructed by Steve Clough (Lila Vodkin lab,
University of Illinois)."

```
                                                              from the recombinant lambda-zap phage using Ex-assist
                                                              helper phage and propagated in XLOLR cells."

BASE COUNT       185 a      167 c     148 g     200 t
ORIGIN

            Query Match          14.3%;     Score 281.2;  DB 10;   Length 700;
            Best Local Similarity   70.0%;     Pred. No. 5.2e-55;
            Matches   423;  Conservative    0; Mismatches 173;  Indels    8;  Gaps    3;

Qy    894  caatcgacactctctccgatactcttcaga-tgcacttctacgagacttgtccttat  952
                |||| |-| |||||| ||||||| |  |||||-| ||||||| || ||  |||||
Db     66  CAATCGATTCATCATTCTCAGAAATTCTCACACTTCTATGAATCTTCACCTTAT  125

Qy    953  ctcaagttcgctcac--ttcacggcgaatcaagcagctttcaagggaagaa  1011
                |||| ||||| |  ||  |-|||  ||| |||||||||||| |||||||||||||
Db    126  CTCAAATTCGCTCACTTTCACTCTGCTAATCAAGCATTCTCGAAGCTTCGCCGGTGCCGG  185

Qy   1012  aagagttcatgtcattgatttctctatgatcaagtctttcaatggccgcgcttatgca  1071
                ||||||||||| ||||| | |||  |  |-||||  |-|||||| ||||||||||||||
Db    186  AAGAGTTCATGTTATAGATTTTGGTCTTAAACAAGGATGCAATGGCCTGCCTTATGCA  245

Qy   1072  ggctcttggcttcgacctggtggtcctcctgtttccgttaaccggaattggtccacc  1131
                |||||||||||||||||||||| |||||||||| |  |||||||||||| || ||
Db    246  AGCGCTGGCATTACGTCCTGGCGGTCCTCCTACGTTCCCGTTAACCGGACCGCC  305

Qy   1132  ggcaccggagataatttcgattatctcatgaagtgtgggtgtaagctggctcattagctga  1191
                ||  ||||||||||| ||| |-|||| ||||||||| |-||||||| ||||| |||| ||
Db    306  GCAGGCGGACAAATACTGATGCTTTGCAACAAGTTGGCTGGAAATTAGCTCAGCTTGCTCA  365

Qy   1192  ggcgattcacgttgagttgagtacagagagatttgtggctcaacacttagctgatcttga  1251
                |-||| ||| || ||||| | |||||||||||||||||  |||||||||||| || ||||
Db    366  GACAATCGGTGTTCAGTTCGAGATTTCGTGGATTTGTTAACAGTATTGCGGATCTTGA  425

Qy   1252  tgcttcgatgctggagcttgagaccaagtgagattgaatctgttgcggttaactcgtttt  1311
                |-||||||| |||||||||| |||||||||||| || |||||  ||||| ||||||
Db    426  CCCGAAATATGCTTGAGATCCGACACCGG-----TGAAGCTGTTGCTGTTAACTCCGTTTT  479

Qy   1312  cgagcttcacaagctcttgggacgacctggtgcgatcgataaggttcttggtggtgaa  1371
                ||||||||||||||| | ||| | ||||||  ||-||||-| || |||-||||| ||
Db    480  CGAGCTTCATACCATGTTAGCTCGACCCGGTTCAGTTGAAGTTCTCAACACTGTTAA  539

Qy   1372  tcagattaaaccggagatttcactgtggttgagcaggaatcgaaccataatagtccgat  1431
                ||| || |||| ||||||||| ||  | || ||-|| || |||||| |||||||||||
Db    540  GAAGATAAACCCTAAAATCGTACCAATCGTTGAGCAAGAAGCGAATCATAACCGACCGGT  599

Qy   1432  tttctagatcggttactgagtcgtcgcattattactccgacgtgtttgactcgttga  1491
                |||||| ||| || |||| | ||| |-|| |-||||||||||||||||-|||| |||||
Db    600  TTTCGTAGACCGGTTACCGAAGCTTTACATTATTACTCAAGCTTATTCGATTCACTGA  659

Qy   1492  aggt  1495
                ||||
Db    660  AGGT  663


RESULT 15
BG452287
LOCUS       BG452287                    686 bp    mRNA     linear    EST 16-MAR-2001
DEFINITION  NF083C09LF1F1070 Developing leaf Medicago truncatula cDNA clone
            NF083C09LF 5', mRNA sequence.
ACCESSION   BG452287
VERSION     BG452287.1   GI:13371081
KEYWORDS    EST.
SOURCE      barrel medic.
ORGANISM    Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 686)
AUTHORS     Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
TITLE       Expressed Sequence Tags from the Samuel Roberts Noble Foundation
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Qy   1188  ctgagcgattcacgttggagtttgagtacagagagatttgtggctaacacttagctgatc  1247
                |-|||  ||| ||| |||||||  ||  ||-||||| || || || ||||| ||||||||
Db    242  CGGAGAGGATCCACGTGCAGTTCGAGTTCGAGTACCGCGGCTTCGTCGCAAAACAGCCTCGCCGATC  301

Qy   1248  ttgatgcttcgatcgctgagccaagtgagattgaatctgtgcggttaactctg  1307
                | |-|| |||||||| ||  ||  ||||||||| || ||| || |||| |||||
Db    302  TCGACGCCTCCATGCTGGATCTCCGA------GAAGACGAGTCCGTGGCGGTGAACTCCG  355

Qy   1308  ttttcgagctcacaagctctgggacgaacctgtgcgatcgataaggttcttggtgtgg  1367
                | |||||||| |||-||||||||| | |-||  ||-||| ||| ||||| || ||  |-|
Db    356  TCTTCGAGTTCACAAGCTCTCGCGCCGCCCGGCGTGGAGAAAGTCCTCTCCGTCG  415

Qy   1368  tgaatcagtataaaccggagatttcactgtggttgagcaggaatcgaaccataatagtc  1427
                ||||   | || ||||||||| ||| ||  | || |||| ||-|||||| |||||||||-|
Db    416  TTCGGCAGATTCGGCCTGAGATCCTCACCGTCGTCGAGCAAGAAGCGAACCACAACGGAC  475

Qy   1428  cgatttcttagatcggtttactgagtcgttgcattattactcgacgtgtttgactcgt  1487
                || |||| || ||| || || || | ||-| ||||| |-|| |||||  ||||| |||||
Db    476  TGAGTTGTGTCGACCGGATCACCGAGTCACTGACTGCAGTCACTCCACTCCTATTCCGACTCGC  535

Qy   1488  tggaaggt  1495
                || |||||
Db    536  TGGAGGGT  543


RESULT 14
BG587404
LOCUS       BG587404                    700 bp    mRNA     linear    EST 11-APR-2001
DEFINITION  EST489176 MHAM Medicago truncatula/Glomus versiforme mixed EST
            library cDNA clone pMHAM-48L4 5' end, mRNA sequence.
ACCESSION   BG587404
VERSION     BG587404.1   GI:13602468
KEYWORDS    EST.
SOURCE      Medicago truncatula/Glomus versiforme mixed EST library.
ORGANISM    Medicago truncatula/Glomus versiforme mixed EST library
            Eukaryota; mixed EST libraries.
REFERENCE   1  (bases 1 to 700)
AUTHORS     Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.
            and Fraser,C.M.
TITLE       ESTs from roots of Medicago truncatula after colonization with
            Glomus versiforme.
JOURNAL     Unpublished (2001)
COMMENT     Contact: Harrison M.J.
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73401
            Tel: 580-223-5810
            Fax: 580-221-7380
            Email: mjharrison@noble.org
            Noble EST name: N386474e TIGR sequence name: MTDDF62TK More
            information is available at: http://www.medicago.org
            Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
FEATURES             Location/Qualifiers
     source          1..700
                     /organism="Medicago truncatula/Glomus versiforme mixed EST
                     library"
                     /cultivar="Medicago truncatula genotype A17"
                     /db_xref="taxon:119092"
                     /clone="pMHAM-48L4"
                     /clone_lib="MHAM"
                     /tissue_type="roots colonized with Glomus versiforme"
                     /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
                     post-inoculation with Glomus versiforme. The library was
                     made from a mixture of RNA from each of these stages."
                     /lab_host="E. coli strain XLOLR"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; cDNA was prepared from polyA+ enriched RNA from
                     roots harvested at 10, 17, 22, 31 and 38 days
                     post-inoculation with Glomus versiforme. The cDNA was
                     directionally ligated into the Unizap XR vector from
                     Stratagene and packaged using Gigapack III Gold packaging
                     extracts. Plasmids containing cDNA inserts were excised
```

```
JOURNAL      Medicago truncatula leaf library
             Unpublished (2000)
COMMENT      Contact: May GD
             Plant Biology Division
             The Samuel Roberts Noble Foundation
             2510 Sam Noble Parkway, Ardmore, OK 73402, USA
             Tel: 580 221 7391
             Fax: 580 221 7380
             Email: gdmay@noble.org
             Insert Length: 686    Std Error: 0.00
             Plate: 083   row: C   column: 09
             Seq primer: TCACACGGAAACAGCTATGAC.
FEATURES     Location/Qualifiers
     source  1..686
             /organism="Medicago truncatula"
             /db_xref="taxon:3880"
             /clone="NF083C09LF"
             /clone_lib="Developing leaf"
             /tissue_type="leaf"
             /dev_stage="Pooled developmental"
             /note="Vector: Lambda Zap; Contains a mixture of very
             young, developing, mature and senescing leaves."
BASE COUNT   183 a        151 c     147 g     199 t     6 others
ORIGIN
```

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Query Match             14.1%;    Score 277.2;  DB 10;   Length 686;
Best Local Similarity   73.4%;    Pred. NO. 4.4e-54;
Matches 384;   Conservative   0;   Mismatches 123;   Indels  16;   Gaps   2;

Qy   663  caactcggccatgtgtcctggttgactcgcaggagaacgtgtgcgtctcgttcacgcgc  722
          !!!!!!! ! !!!!! !! ! !!!!!!! !!!!  !!!!!!!! ! !!!! !!!!!
Db   164  CAACTCGTCCTATAATGCTGCTGGAGACACAAGAGAAAAGGTATTCGTCTCGTTCATAGTT  223

Qy   723  ttttggcttgcgctgaagctgttcagagaggagaatctgactgtggcggaagctctggtga  782
          ! !!!!!!!!! !!!!!!!!!  !! ! !!!!! !! ! !!!!  ! !!!!!! !!!!!
Db   224  TGATGGCTTGTGCTGAAGCTGTTGAACAGAATAATCTAAAGATGGCGGAGGCTTTGGTTA  283

Qy   783  agcaaatcggattcttagctgttttccaaatcggagctatgagaaaagtcgctacttact  842
          ! !! !!!!!!!! !!!!!!!!!!  !!  !! !!  !! !!!!!!!!!!! !! !! !!
Db   284  AACAGATCGGATACTTAGCTGTATCACAAGAAGGTGCTATGAGAAAAGTTGCAACCTATT  343

Qy   843  tcgccgaagctctcgcgcggcggcggattaccgtctctccgtctcgtcgcagagtccaatcgacc  902
          !!!! !!!! !!! !  !!!!  !! ! !!! !!!!!!!!!! !! !! !!!!!
Db   344  TCGCTGAAGGTTTAGCTAGGAGAATCTACCGTGTGTTTCC---------ACAGC  388

Qy   903  actctctccgatactcttcagatgcacttctacgagacttgtccttatctcaagttcg  962
          ! ! !!!!!! ! !!!!!!! !! !!!!! !! !!!!!!!!! !!!!! !! !!!!!
Db   389  ATTCCGTTCCGATTCACTTCAGATCCATTTCTATGAAACTTGTCCTAATCTAAAATTCG  448

Qy   963  ctcacttcacgcgaatcaagcgattctcgaagctttcaagggaagaaagagttcatg  1022
          !!!!!!!!!! !!!!!!!!! !! !!!!!!!!!!!!!!  !! !!!!!!!! !!!!!!!
Db   449  CTCACTTCACTGCGAATCAAGCTATTCTAGAAGCTTTTCAAGGAAAAATCTAGTGTTCATG  508

Qy   1023 tcattgatttctctcatgagtcaagtctttcaatgccggcggctcatgcaggctcttgcgc  1082
          !!!!!!!!!! !!!!!!!!!!!!!! !!! !!! !!! ! !!!!!!!!!!!!!!
Db   509  TGATTGATTTCTCGATTAATCAAGGATGCAGTGGCCGGCGCCTTATGCAGGCACTTGCTT  568

Qy   1083 ttcgacctggtggtcctccctgttttccggttaaccggattggtccaccggcaccggata  1142
          ! !!! !!!!!!!!!!!!!!! !!! !!!!!  !! !!!!!!! !! !!!  !!!! !!!!!
Db   569  TACGTCCTGGTGGTCCTCCTGCTTTTCGGNTGACCGGAATCGGACCTNCGGCGTCGGATA  628

Qy   1143 atttcgattatcttcatgaagttgggtgtaagctgctcattt  1185
          ! ! ! !! !!!!!!!! !!!!!!!!!! ! !!! !!!!!!!!
Db   629  A-CTANATCATTTNNACAAGTTGGGTGGAGGCTTGCTCATTT  670
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Search completed: May 11, 2002, 16:02:11
Job time: 4472 sec